EXHIBIT 9

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                                                                    ATGTC
-145
-140   CATGAACTGC TGAGTGGATA AACAGCACGG GATATCTCTG TCTAAGGAA TATTACTACA CCAGGAAAAG
-70    GACACATTCG ACAACAGGAA AGGAGCCTGT CACAGAAAAC CACAGTGTCC TGTGCATGTG ACATTCGCC
 1     ATG GGA AAC AAC TGT TAC AAC GTG GTG GTC ATT GTG CTG CTG CTA GTG GGC TGT GAG AAG   60
 1     Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Leu Val Gly Cys Glu Lys   20

 61    GTG GGA GCC GTG CAG AAC TCC TGT GAT AAC TCT CAG CCT GGT ACT TTC TGC AGA AAA TAC   120
 21    Val Gly Ala Val Gln Asn Ser Cys Asp Asn Lys Gln Pro Gly Thr Phe Cys Arg Lys Tyr   40

 121   AAT CCA GTC TGC AAG AGC TGC CCT CCA AGT AGC TTG TCC AGC ATA GGT GGA CAG CCG AAC   180
 41    Asn Pro Val Cys Lys Ser Cys Pro Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn   60

 181   TGT AAC ATC TGC AGA GTG TGT GCA GGC TAT TTC AGG TTC AAG AAG TTT TGC TCC TCT ACC   240
 61    Cys Asn Ile Cys Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr   80

 241   CAC AAC GCG GAA TGT GAG TGC ATT GAA GGA TTC CAT TGC TTG GGG CCA CAG TGC ACC AGA   300
 81    His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro Gln Cys Thr Arg   100

 301   TGT GAA AAG GAC TGC AGG CCT GGC CAG GAG CTA ACG AAG CAG GGT TGC AAA ACC TGT AGC   360
 101   Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr Lys Gln Gly Cys Lys Thr Cys Ser   120

 361   TTG GGA ACA TTT AAT GAC CAG AAC GGT ACT GGC GTC TGT CGA CCC TGG ACG AAC TGC TCT   420
 121   Leu Gly Thr Phe Asn Asp Gln Asn Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser   140

 421   CTA GAC GGA AGG TCT GTG CTT AAG ACC GGG ACC ACG GAG AAG GAC GTG GTG TGT GGA CCC   480
 141   Leu Asp Gly Arg Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro   160

 481   CCT GTG GTG AGC TTC TCT CCC AGT ACC ACC ATT TCT GTG ACT CCA GAG GGA GGA CCA GGA   540
 161   Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu Gly Gly Pro Gly   180

 541   GGG CAC TCC TTG CAG GTC CTT ACC TTG TTC CTG GCG CTG ACA TCG GCT TTG CTG CTG GCC   600
 181   Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu Ala Leu Thr Ser Ala Leu Leu Leu Ala   200

 601   CTG ATC TTC ATT ACT CTC CTG TTC TCT GTG CTC AAA TGG ATC AGG AAA AAA TTC CCC CAC   660
 201   Leu Ile Phe Ile Thr Leu Leu Phe Ser Val Leu Lys Trp Ile Arg Lys Lys Phe Pro His   220

 661   ATA TTC AAG CAA CCA TTT AAG AAG ACC ACT GGA GCA GCT CAA GAG GAA GAT GCT TGT AGC   720
 221   Ile Phe Lys Gln Pro Phe Lys Lys Thr Thr Gly Ala Ala Gln Glu Glu Asp Ala Cys Ser   240

 721   TGC CGA TGT CCA CAG GAA GAA GAA GGA GGA GGA GGA GGC TAT GAG CTG TGA TGTACTATC   780
 241   Cys Arg Cys Pro Gln Glu Glu Glu Gly Gly Gly Gly Gly Tyr Glu Leu ---

 781   CTAGGAGATG TGTGGGCCGA AACCGAGAAG CACTAGGACC CCACCATCCT GTGGAACAGC ACAAGCAACC   850
 851   CCACCACCCT GTTCTTACAC ATCATCCTAG ATGATGTGTG GGCGCGCACC TCATCCAAGT CTCTTCTAAC   920
 921   GCTAACATAT TTGTCTTTAC CTTTTTTAAA TCTTTTTTTA AATTTAAATT TTATGTGTGT GAGTGTTTTG   990
 991   CCTGCCTGTA TGCACACGTG TGTGTGTGTG TGTGTGTGAC ACTCCTGATG CCTGAGGAGG TCAGAAGAGA   1060
 1061  AAGGGTTGGT TCCATAACAA CTGGAGTTAT GGATGGCTGT GAGCCGGnnn GATAGGTGGG GACGGAGACC   1130
 1131  TGTCTTCTTA TTTTAACGTG ACTGTATAAT AAAAAAAAAA TGATATTTCG GGAATTGTAG AGATTGTCCT   1200
 1201  GACACCCTTC TAGTTAATGA TCTAAGAGGA ATTGTTGATA CGTAGTATAC TGTATATGTG TATGTATATG   1270
 1271  TATATGTATA TATAAGACTC TTTTACTGTC AAAGTCAACC TAGAGTGTCT GGTTACCAGG TCAATTTTAT   1340
 1341  TGGACATTTT ACGTCACACA CACACACACA CACACACACA CACGTTTATA CTACGTACTGT TATCGGTAT   1410
 1411  TCTACGTCAT ATAATGGGAT AGGGTAAAAG GAAACCAAAG AGTGAGTGAT ATTATTGTGGA GGTGACAGA   1480
 1481  CTACCCCTTC TGGGTACGTA GGGACAGACC TCCTTCGGAC TGTCTAAAAC TCCCCTTAGA AGTCTCGTCA   1550
 1551  AGTTCCCGGA CGAAGAGGAC AGAGGAGCAA CAGTCCGAAA AGTTATTTTT CCGGCAAATC CTTTCCCTGT   1620
 1621  TTCGTGACAC TCCACCCCTT GTGGACACTT GAGTGTCATC CTTCGCGCCGG AAGGTCAGGT GGTACCCGTC   1690
 1691  TGTAGGGGCG GGAGACAGA GCCGCGGGGG AGCTACGAGA ATCGACTCAC AGGGCGCCCC GGGCTTCGCA   1760
 1761  AATGAAACTT TTTTAATCTC ACAAGTTTCG TCCGGGCTCG GCGGACCTAT GGCGTCGATC CTTATTACCT   1830
 1831  TATCCTGGCG CCAAGATAAA ACAACCAAAA GCCTTGACTC CGGTACTAAT TCTCCCTGCC GGCCCCCGTA   1900
 1901  AGCATAACGC GGCGATCTCC ACTTTAAGAA CCTGGCCGCG TTCTGCCTGG TCTCGCTTTC GTAAACGGTT   1970
 1971  CTTACAAAAG TAATTAGTTC TTGCTTTCAG CCTCCAAGCT TCTGCTAGTC TATGGCAGCA TCAAGGCTGG   2040
 2041  TATTTGCTAC GGCTGACCGC TACGCCGCCG CAATAAGGGT ACTGGGCGGC CCGTCGCAAGG CCCTTTGGTT   2110
 2111  TCAGAAACCC AAGGCCCCCC TCATACCAAC GTTTCGACTT TGATTCTTGC CGGTACGTGG TGGTGGGTGC   2180
 2181  CTTAGCTCTT TCTCGATAGT TAG AC
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